



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/753,750B

DATE: 10/17/2002
TIME: 10:12:36

Input Set : A:\08753750_seqlisting.txt
Output Set: N:\CRF4\10172002\H753750B.raw

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OCT 30 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: Lo, Reggie Y.C.
 5 Schryvers, Anthony B.
 6 Potter, Andrew A.
 8 <120> TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
 9 PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
 12 <130> FILE REFERENCE: A34762 021645.0105
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/08/753,750B
 15 <141> CURRENT FILING DATE: 1996-11-29
 17 <150> PRIOR APPLICATION NUMBER: CA 2,164,274
 18 <151> PRIOR FILING DATE: 1995-12-01
 20 <150> PRIOR APPLICATION NUMBER: 60/008,569
 21 <151> PRIOR FILING DATE: 1995-12-01
 23 <160> NUMBER OF SEQ ID NOS: 68
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2793
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Pasteurella haemolytica
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: 2544
 35 <223> OTHER INFORMATION: a, c, g or t
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 39 ctttcgtcatt catacgggtgc tgccactgaa aataaaaaaaa tcgaagaaaa taacgatcta 120
 40 gctgttctgg atgaaggttat tggacagag agccattatg ctcacgaacg tcaaaacgaa 180
 41 gtaactggct tggggaaaagt agtggaaaaat tatcacgaaa tggataaaaa tcaaattctt 240
 42 ggtattcgtg atttaactcg ctatgaccct ggtatttcgg tgggtggaaaca aggtcgcgg 300
 43 gcaagtagtg gctatgccat tcgagggtgtt gataaaaaacc gtgtcagctt acttgttgc 360
 44 gggctaccac aagcgcacag ttatcatacg ctaggttcag atgctaattgg tgggtcaatt 420
 45 aatgagattt agtatgaaaaa cattcggtca attgagttaa gcaaaggagc aagttctgcg 480
 46 gaatatggct ctggcgca tgggtggctt attgggtttc gtactaaaga tgcgcaggat 540
 47 attattaaag aggggcagca ttggggctta gatagtaaga cctcttatgc cagaaaaaat 600
 48 agccatttt tacagtctat cgccagcggct ggtgaggcgg gtgggtttga agcacttgc 660
 49 attgcaactc accgacacgg taaagagacc aaaattcatt ccgaggcaaa taaattaaaa 720
 50 cataatattc ggcgtataac cgccgttggaa aatcgctacg actttaccctt aattccgcac 780
 51 agaatgctcc tggaggatct ccttttaattt gtggaaagata cttggcccaac attagattgt 840
 52 actcctcggt caagggttaa gtgtaccgc gataattcc cagtgagaac atttccggaa 900
 53 tatacgcctg aagagcgc当地 aacagcttgcg cagatccctt atcgactgaa gcagctctca 960
 54 gcccaagaat ataccggtaa agatcgccattt gcacccaaacc ctttagatca caagatgtt 1020
 55 tctgtttta tgaagttgg ctatcactt aactcgctc attatcttgg cgcaatctt 1080
 56 gaagatacaa aaacacgctt cgtatccgtt gatatgcaaa cgccagctt ctataaaaa 1140
 57 gacgatatta acttataactt taggaactat gttatgaaag gggataatat tttatggc 1200

P.6
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58 tttagtgttca agccaaggat cccttatggg ttgcgctata gccatgtgaa gtttttgat 1260
 59 gaacgtcacc acaaacgtcg tttaggattc acctataaat ataaaccaga gaataatcgc 1320
 60 tgggtggata gcattaaact cagtgcggat aaacaagata ttagaactata tagccggcta 1380
 61 catcgcttgc attgttagcga ttatcctgtg gtagataaaa attgccgccc gactttggat 1440
 62 aaatcttggt ctatgtatcg aactgagcgt aataattacc aagaaaagca tcgtgtcatt 1500
 63 catttagaat ttgataaaagc gctaaatgct ggtcaaggcg tatttaacca aacccacaaa 1560
 64 ctgaatttag gggtgggctt tgatcgattt aattcgctta tggatcatgg ggatatgact 1620
 65 gcccaatata ccaaaggcgg ttataccagg taccgcggta gagggcggtt agataatcca 1680
 66 tatattttatc gccgcgatcc acgcgttattt gaaacggtat ctttgcgtaa taatacacgc 1740
 67 ggcacatct taaactgtga accgcgtaaa attaaaggcg atagccattt tgtagcttc 1800
 68 cgcgatctag tgataaagcga gtatgtggat ttgggattag ggggtgcgtt tgatcaacat 1860
 69 cgatttaat ctgatgatcc gtggacactt agccgaactt atcgaaattt gtcttggat 1920
 70 ggtgggatta cgcttaaacc aacagagttt gtatcgctt cttatcgcat ttcaaacgg 1980
 71 ttttagagtgc ctgcattcta tgaactttat ggttaaacgtg atcatattgg gcttaaagat 2040
 72 aacaataatg tgcAACCGCg cAACACGTAG caccagttt agccagaaaa atcgactaat 2100
 73 catgagattt gagttagctt taaaggtcaa tttgggtacc ttgatgttag ctattccgt 2160
 74 aataactata aaaatatgtat tgacgacagca tgtaaaagaa taatacaaaa atcacactgt 2220
 75 ttctataact accataataat tcaagatgtg gcactaaacg ggataaattt agtcgctaaa 2280
 76 ttgacttac acggattttt atctatgtcg ccagatgggtt tttatttcattt agttgcttat 2340
 77 aaccgtgtaa aagtaaaaga gcccggaaacta accgactcaa gactcgatag cgtaaacgat 2400
 78 cctattctag atgcattca gccaggcacgc tatgtgcattt gattcggctt cgcattcccc 2460
 79 gaagaaaaat ggggaaattgg cattactacc acctattcta aagccaaaaa cggccgatgag 2520
 W--> 80 gtggcaggca cacgtcatca cggnatatacat cgcgttgatt taggtggcaa actgaccggt 2580
 81 tcttggtaca cccatgatata taccgggttac atcaattata aaaactacac cttacgtgga 2640
 82 ggaattttata atgtgactaa tcgtaaatata tccacttggg aatcgtgcg ccaatccgg 2700
 83 gtgaatgcag taaaccaaga cccgggttagc aattacactc gatttggcgc tccggggaga 2760
 84 aatttcagtt tagcatttga aatgaagttt tag 2793
 86 <210> SEQ ID NO: 2
 87 <211> LENGTH: 930
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Pasteurella haemolytica
 91 <400> SEQUENCE: 2
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 93 1 5 10 15
 94 Val Leu Phe Ala Leu Ser His Ser Tyr Gly Ala Ala Thr Glu Asn Lys
 95 20 25 30
 96 Lys Ile Glu Glu Asn Asn Asp Leu Ala Val Leu Asp Glu Val Ile Val
 97 35 40 45
 98 Thr Glu Ser His Tyr Ala His Glu Arg Gln Asn Glu Val Thr Gly Leu
 99 50 55 60
 100 Gly Lys Val Val Lys Asn Tyr His Glu Met Ser Lys Asn Gln Ile Leu
 101 65 70 75 80
 102 Gly Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu
 103 85 90 95
 104 Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ala Ile Arg Gly Val Asp Lys
 105 100 105 110
 106 Asn Arg Val Ser Leu Leu Val Asp Gly Leu Pro Gln Ala His Ser Tyr
 107 115 120 125
 108 His Thr Leu Gly Ser Asp Ala Asn Gly Gly Ala Ile Asn Glu Ile Glu

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109	130	135	140
110	Tyr Glu Asn Ile Arg Ser Ile Glu Leu Ser Lys Gly Ala Ser Ser Ala		
111	145	150	155
112	Glu Tyr Gly Ser Gly Ala His Gly Gly Ala Ile Gly Phe Arg Thr Lys		160
113	165	170	175
114	Asp Ala Gln Asp Ile Ile Lys Glu Gly Gln His Trp Gly Leu Asp Ser		
115	180	185	190
116	Lys Thr Ser Tyr Ala Ser Lys Asn Ser His Phe Leu Gln Ser Ile Ala		
117	195	200	205
118	Ala Ala Gly Glu Ala Gly Gly Phe Glu Ala Leu Val Ile Ala Thr His		
119	210	215	220
120	Arg His Gly Lys Glu Thr Lys Ile His Ser Glu Ala Asn Lys Leu Lys		
121	225	230	235
122	His Asn Ile Arg Arg Ile Thr Gly Phe Glu Asn Arg Tyr Asp Phe Thr		
123	245	250	255
124	Gln Ile Pro His Arg Met Leu Leu Glu Asp Leu Leu Leu Ile Val Glu		
125	260	265	270
126	Asp Thr Cys Pro Thr Leu Asp Cys Thr Pro Arg Ala Arg Val Lys Leu		
127	275	280	285
128	Asn Arg Asp Asn Phe Pro Val Arg Thr Phe Pro Glu Tyr Thr Pro Glu		
129	290	295	300
130	Glu Arg Lys Gln Leu Glu Gln Ile Pro Tyr Arg Thr Glu Gln Leu Ser		
131	305	310	315
132	Ala Gln Glu Tyr Thr Gly Lys Asp Arg Ile Ala Pro Asn Pro Leu Asp		
133	325	330	335
134	Tyr Lys Ser Asn Ser Val Phe Met Lys Phe Gly Tyr His Phe Asn Ser		
135	340	345	350
136	Ser His Tyr Leu Gly Ala Ile Leu Glu Asp Thr Lys Thr Arg Tyr Asp		
137	355	360	365
138	Ile Arg Asp Met Gln Thr Pro Ala Tyr Tyr Thr Lys Asp Asp Ile Asn		
139	370	375	380
140	Leu Ser Leu Arg Asn Tyr Val Tyr Glu Gly Asp Asn Ile Leu Asp Gly		
141	385	390	395
142	Leu Val Phe Lys Pro Arg Ile Pro Tyr Gly Leu Arg Tyr Ser His Val		
143	405	410	415
144	Lys Phe Phe Asp Glu Arg His His Lys Arg Arg Leu Gly Phe Thr Tyr		
145	420	425	430
146	Lys Tyr Lys Pro Glu Asn Asn Arg Trp Leu Asp Ser Ile Lys Leu Ser		
147	435	440	445
148	Ala Asp Lys Gln Asp Ile Glu Leu Tyr Ser Arg Leu His Arg Leu His		
149	450	455	460
150	Cys Ser Asp Tyr Pro Val Val Asp Lys Asn Cys Arg Pro Thr Leu Asp		
151	465	470	475
152	Lys Ser Trp Ser Met Tyr Arg Thr Glu Arg Asn Asn Tyr Gln Glu Lys		
153	485	490	495
154	His Arg Val Ile His Leu Glu Phe Asp Lys Ala Leu Asn Ala Gly Gln		
155	500	505	510
156	Gly Val Phe Asn Gln Thr His Lys Leu Asn Leu Gly Leu Gly Phe Asp		
157	515	520	525

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158 Arg Phe Asn Ser Leu Met Asp His Gly Asp Met Thr Ala Gln Tyr Thr
159 530 535 540
160 Lys Gly Gly Tyr Thr Ser Tyr Arg Gly Arg Gly Arg Leu Asp Asn Pro
161 545 550 555 560
162 Tyr Ile Tyr Arg Arg Asp Pro Arg Ser Ile Glu Thr Val Ser Leu Cys
163 565 570 575
164 Asn Asn Thr Arg Gly Asp Ile Leu Asn Cys Glu Pro Arg Lys Ile Lys
165 580 585 590
166 Gly Asp Ser His Phe Val Ser Phe Arg Asp Leu Val Ile Ser Glu Tyr
167 595 600 605
168 Val Asp Leu Gly Leu Gly Val Arg Phe Asp Gln His Arg Phe Lys Ser
169 610 615 620
170 Asp Asp Pro Trp Thr Leu Ser Arg Thr Tyr Arg Asn Trp Ser Trp Asn
171 625 630 635 640
172 Gly Gly Ile Thr Leu Lys Pro Thr Glu Phe Val Ser Leu Ser Tyr Arg
173 645 650 655
174 Ile Ser Asn Gly Phe Arg Val Pro Ala Phe Tyr Glu Leu Tyr Gly Lys
175 660 665 670
176 Arg Asp His Ile Gly Leu Lys Asp Asn Glu Tyr Val Gln Arg Ala Gln
177 675 680 685
178 Arg Ser His Gln Leu Glu Pro Glu Lys Ser Thr Asn His Glu Ile Gly
179 690 695 700
180 Val Ser Phe Lys Gly Gln Phe Gly Tyr Leu Asp Val Ser Tyr Phe Arg
181 705 710 715 720
182 Asn Asn Tyr Lys Asn Met Ile Ala Thr Ala Cys Lys Arg Ile Ile Gln
183 725 730 735
184 Lys Ser His Cys Phe Tyr Asn Tyr His Asn Ile Gln Asp Val Ala Leu
185 740 745 750
186 Asn Gly Ile Asn Leu Val Ala Lys Phe Asp Leu His Gly Ile Leu Ser
187 755 760 765
188 Met Leu Pro Asp Gly Phe Tyr Ser Ser Val Ala Tyr Asn Arg Val Lys
189 770 775 780
190 Val Lys Glu Arg Lys Leu Thr Asp Ser Arg Leu Asp Ser Val Asn Asp
191 785 790 795 800
192 Pro Ile Leu Asp Ala Ile Gln Pro Ala Arg Tyr Val Leu Gly Phe Gly
193 805 810 815
194 Tyr Asp His Pro Glu Glu Lys Trp Gly Ile Gly Ile Thr Thr Thr Tyr
195 820 825 830
196 Ser Lys Ala Lys Asn Ala Asp Glu Val Ala Gly Thr Arg His His Gly
197 835 840 845
198 Ile His Arg Val Asp Leu Gly Gly Lys Leu Thr Gly Ser Trp Tyr Thr
199 850 855 860
200 His Asp Ile Thr Gly Tyr Ile Asn Tyr Lys Asn Tyr Thr Leu Arg Gly
201 865 870 875 880
202 Gly Ile Tyr Asn Val Thr Asn Arg Lys Tyr Ser Thr Trp Glu Ser Val
203 885 890 895
204 Arg Gln Ser Gly Val Asn Ala Val Asn Gln Asp Arg Gly Ser Asn Tyr
205 900 905 910
206 Thr Arg Phe Gly Ala Pro Gly Arg Asn Phe Ser Leu Ala Phe Glu Met

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207	915	920	925
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209	930		
212	<210> SEQ ID NO: 3		
213	<211> LENGTH: 1755		
214	<212> TYPE: DNA		
215	<213> ORGANISM: Pasteurella haemolytica		
217	<400> SEQUENCE: 3		
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219	tcaaatggtg gaagcttga tggtaatct gccaaggatg aatctcaaac gcaaactacc	120	
220	ccccaaaagc caagtttaca agatgataat agtaacgcaa gacgtacagt aagcgcttct	180	
221	gaaaactgaag ctttattgca gccggggttt gggttttcag cccaaaattcc gcgtcgtaat	240	
222	ctccttccgc aggggaagga agatgttagcc cctattggtg atataaaaaga gattactgga	300	
223	gatctgcca aaattccgta tgaagaagag gttaaagcgt gcggtagtag tgctgatgga	360	
224	tttagccata ctcatgatag aaatcataag ttgtatacaa gagattttaa ttttgttcgt	420	
225	tccggctatg ttgtgcattc tggtccaaaa cctgaaataa agcctaaaga aattttgaga	480	
226	acaggtgcac atgggtatgt ttactattt ggtatagagc cgcggaaagc aataacctacc	540	
227	caaaaactaa cttataaagg atattggat tttactaccc atgcggctaa ggggagagat	600	
228	agtaatattt ttctaattcc cgcaggcatc aatagtggcg ccataccgga aaatagtac	660	
229	gatattaatg ttgatgattc tggaaaaacca atggggcata caggagaatt tacggctgat	720	
230	tttgctaata aaactttaac tggAACATTG gttcgtaatg ggtatgttag tcgttagcaa	780	
231	gagaaaaaaaaa ttacaacaat ttacgatatt gatgcgaaaa ttAAAGGTAA tcgctttct	840	
232	ggtaaagcaa accaaaaaaaaa accgatgatc cttatTTTg ggaaaagctc cacgacactt	900	
233	gaaggtggat ttttgggtgg ggaggctcaa gaacttgcgg gtaaattctt agctgtatgt	960	
234	aagtccgtat ttgttggTTT tgctggcaca cgagatgcta aaaaagatga tagtgaatct	1020	
235	gcctttgatg ctttcccaat taaacttaaa gattaaata aatctgagat ggatactttc	1080	
236	ggaaatgcga cacattgtat tattaacaat aagcagattc cacttattgc ggaagccaca	1140	
237	aaaagctttg ccgagatgaa atttgatgat ttggTTACCC gtactattga tggaaaaacg	1200	
238	tatcgagttt cagtcgtcgt taataatttta gattatgtca aatttggat ttatagcgag	1260	
239	ggaaataata gtgatactgc tctccaagaa tatttagtag gagaacgtac agctctggca	1320	
240	gatttgcCAA cagggacagt aaaatatcga ggtacttggg acggggtaat gtacagtaaa	1380	
241	tctggctcgg caggggttga atcgccaagt aacagcgaaa gtggactcg ttcaatttc	1440	
242	gatgttagatt ttgtcaataa aaaaattaat ggcaagctga ttgctaata gttgttggaa	1500	
243	gaacGCCAA tgctgacact ggaaggcaat ctgaaaggga atggTTTgg aggacagcc	1560	
244	aaaacggca attctggTT taatcttgc cccaaaagta cgaatggTgg cacggtaggg	1620	
245	catataaata ctcatttga agggggctt tatggcccta aggcgacgga attaggtgg	1680	
246	attgtacaaa atacagaaac ggataaaagat agagtacgta ttacattcgg cgaaaaacgt	1740	
247	caaataaaaaa aataaa	1755	
249	<210> SEQ ID NO: 4		
250	<211> LENGTH: 584		
251	<212> TYPE: PRT		
252	<213> ORGANISM: Pasteurella haemolytica		
254	<400> SEQUENCE: 4		
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256	1 5 10 15		
257	Ala Ala Cys Ser Ser Asn Gly Gly Ser Phe Asp Val Gln Ser Ala Lys		
258	20 25 30		
259	Val Glu Ser Gln Thr Gln Thr Pro Lys Lys Pro Ser Leu Gln Asp		
260	35 40 45		

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2544
Seq#:28; N Pos. 3,6,7,9,12,15
Seq#:29; N Pos. 11,17,20
Seq#:31; N Pos. 3,6,9,12